

RAW SEQUENCE LISTING

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Application Serial Number: 101829,427
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RAW SEQUENCE LISTING
PATENT APPLICATION: US/10/829,427

DATE: 10/18/2004
TIME: 09:59:19

Input Set : A:\252202US0.txt
Output Set: N:\CRF4\09282004\J829427.raw

3 <110> APPLICANT: FURUKAWA, KEISUKE
 4 KAJIYAMA, NAOKI
 6 <120> TITLE OF INVENTION: MODIFIED SARCOSINE OXIDASES, GENES AND
 RECOMBINANT DNAs THEREOF,
 7 AND METHODS FOR PREPARING THE SAME
 9 <130> FILE REFERENCE: 252202US0
 11 <140> CURRENT APPLICATION NUMBER: 10/829,427
 12 <141> CURRENT FILING DATE: 2004-04-22
 14 <150> PRIOR APPLICATION NUMBER: JP 2003-121533
 15 <151> PRIOR FILING DATE: 2003-04-25
 17 <150> PRIOR APPLICATION NUMBER: JP 2003-396807
 18 <151> PRIOR FILING DATE: 2003-11-27
 20 <150> PRIOR APPLICATION NUMBER: JP 2004-116345
 21 <151> PRIOR FILING DATE: 2004-04-12
 23 <160> NUMBER OF SEQ ID NOS: 4
 25 <170> SOFTWARE: PatentIn version 3.3
 27 <210> SEQ ID NO: 1
 28 <211> LENGTH: 387
 29 <212> TYPE: PRT
 30 <213> ORGANISM: Artificial Sequence
 32 <220> FEATURE:
 33 <223> OTHER INFORMATION: Synthetic Peptide
 35 <400> SEQUENCE: 1
 37 Met Ser Thr His Phe Asp Val Ile Val Val Gly Ala Gly Ser Met Gly
 38 1 5 10 15
 41 Met Ala Ala Gly Tyr Tyr Leu Ala Lys Gln Gly Val Lys Thr Leu Leu
 42 20 25 30
 45 Val Asp Ala Phe Asp Pro Pro His Thr Glu Gly Ser His His Gly Asp
 46 35 40 45
 49 Thr Arg Ile Ile Arg His Ala Tyr Gly Glu Gly Arg Lys Tyr Val Pro
 50 50 55 60
 53 Phe Ala Leu Arg Ala Gln Glu Leu Trp Tyr Glu Leu Glu Asn Glu Thr
 54 65 70 75 80
 57 His Asn Lys Ile Phe Thr Lys Thr Gly Val Leu Val Phe Gly Pro Lys
 58 85 90 95
 61 Gly Glu Ser Asp Phe Val Ala Glu Thr Met Glu Ala Ala Glu His
 62 100 105 110
 65 Ser Leu Thr Val Asp Leu Leu Glu Gly Asp Glu Ile Asn Thr Arg Trp
 66 115 120 125
 69 Pro Gly Ile Thr Val Pro Glu Asn Tyr Asn Ala Ile Phe Glu Pro Asn
 70 130 135 140
 73 Ser Gly Val Leu Phe Ser Glu Asn Cys Ile Arg Ser Tyr Arg Glu Leu
 74 145 150 155 160
 77 Ala Val Ala Lys Gly Ala Lys Ile Leu Thr Tyr Thr Arg Val Glu Asp

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78	165	170	175
81	Phe Glu Val Ser Gln Asp Gln Val Lys Ile Gln Thr Ala Asn Gly Ser		
82	180	185	190
85	Tyr Thr Ala Asp Lys Leu Ile Val Ser Met Gly Ala Trp Asn Ser Lys		
86	195	200	205
89	Leu Leu Ser Lys Leu Asn Leu Asp Ile Pro Leu Gln Pro Tyr Arg Gln		
90	210	215	220
93	Val Val Gly Phe Phe Asp Ser Asn Glu Ala Lys Tyr Ser Asn Asp Val		
94	225	230	235
97	240	Gly Tyr Pro Ala Phe Met Val Glu Val Pro Lys Gly Ile Tyr Tyr Gly	
98	245	250	255
101	Phe Pro Ser Phe Gly Gly Cys Gly Leu Lys Ile Gly Tyr His Thr Tyr		
102	260	265	270
105	Gly Gln Gln Ile Asp Pro Asp Thr Ile Asn Arg Glu Phe Gly Ala Tyr		
106	275	280	285
109	Gln Glu Asp Glu Ser Asn Leu Arg Asp Phe Leu Glu Lys Tyr Met Pro		
110	290	295	300
113	Glu Ala Asn Gly Glu Leu Lys Arg Gly Ala Val Cys Met Tyr Thr Lys		
114	305	310	315
117	320	Gly Pro Asp His His Phe Val Ile Asp Thr His Pro Glu His Ser Asn	
118	325	330	335
121	Val Phe Val Ala Ala Gly Phe Ser Gly His Gly Phe Lys Phe Ser Ser		
122	340	345	350
125	Val Val Gly Glu Val Leu Ser Gln Leu Ala Thr Thr Gly Lys Thr Glu		
126	355	360	365
129	His Asp Ile Ser Ile Phe Ser Ile Asn Arg Pro Ala Leu Lys Gln Lys		
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133	Thr Thr Ile		
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150	acagaaggaa gccatcacgg tgatactcgcc attatccccc atgcctacgg tgaaggaaga 180		
152	aatatgttc catttgact aagagcacaa gaattatgtt atgaacttga aaatgaaaca 240		
154	cacaataaga ttttacaaa aacaggcggtt ctatgttttgcgtt gtccgaaagg tgaatccgat 300		
156	ttcggtgcgc aaacaatggc ggcagctgca gaacattcat tgatcggtt tttacttgcgtt 360		
158	ggtgatgaaa tcaatacgccg ctggcccgcc ataacgggtt ctgaaaacta taatgcatt 420		
160	tttgcgttgcgtt attgttgcgtt gataattgtt ttcgttgcgtt ccgtgatgtt 480		
162	gctgtatgaaa aaggagcaaa aatgtttaaca tataactcggtt ttgaggattt tgaatttttct 540		
164	caagaccaag taaaatcca aacggcaaat ggatcgatca cagctgataa attaattcgta 600		
166	agtatgggtt cttggatatt taaactactt tctaaattaa atcttgacat cccattacag 660		
168	ccataaccgcc aagttgttagg atttttgtt tctaatttttttgcgtt caaagtacag caatgttg 720		
170	gattatccat cattcatgtt agaagtacca aaaggttattt attacggatt cccaaatgtt 780		

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172 ggtggctgcg gtttggaaat agggtatcat acgtatggc aacaaatcga ccctgatacg	840
174 attaaccgtg aatttggtgc ttatcaagag gatgaaaagta atcttcgcga tttcttggaa	900
176 aaatatatgc cagaagcaaa tggcgagttt aaacgaggcg cagcttgtat gtacacgaaa	960
178 acaccagatg aacatttcggtt gattgatact catccagaac attccaatgt tttcgtagca	1020
180 gctggttct ctggcacacgg ctttaaattt tcaagtgttag tcggtaagt gttaagtcaa	1080
182 ttagcgacaa caggtaaaac agaacatgtat atttcaattt tctcaataaa tcgtcctgct	1140
184 ttaaaacaga aaacaacgtat ttaa	1164
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188 <211> LENGTH: 22	
189 <212> TYPE: DNA	
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192 <220> FEATURE:	
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205 <223> OTHER INFORMATION: Synthetic DNA	
207 <400> SEQUENCE: 4	
208 cgacggccag agatctacta g	21

VERIFICATION SUMMARY
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